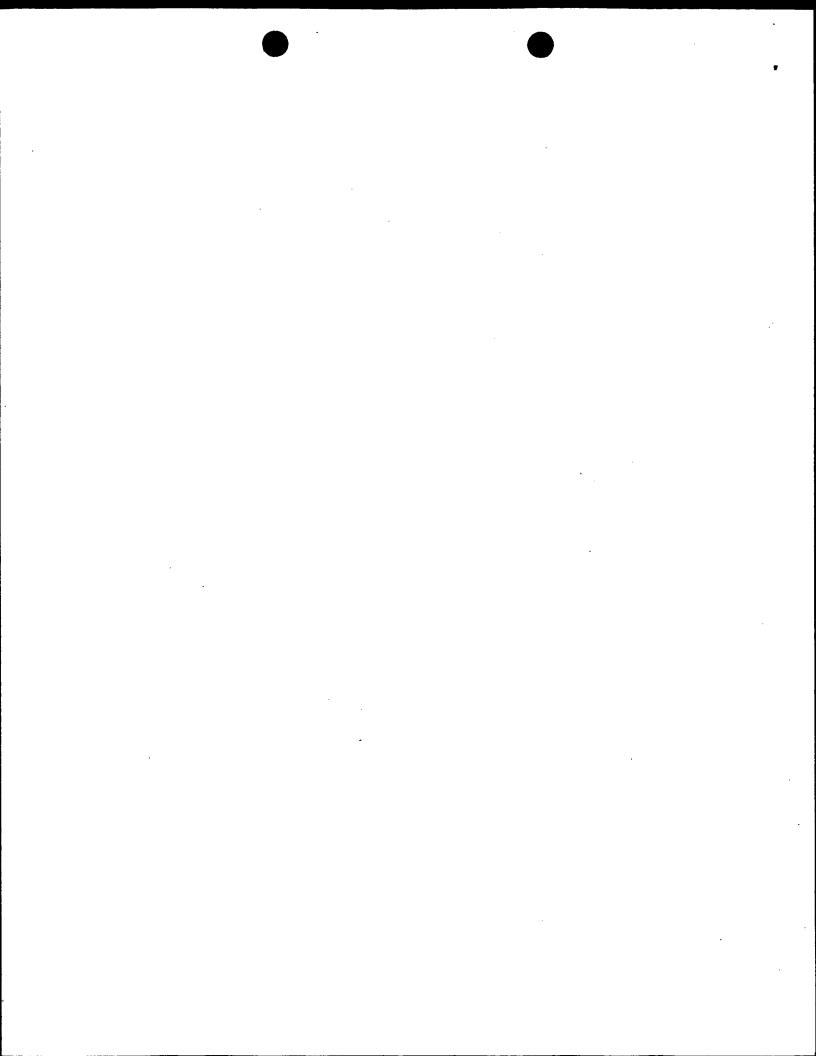
OY  557 AAAAAAAGCTGGAAAAAGAAGAAGAAGAATAAGAGCCAGCTTGTAAAGAAGAAGAGCTGTGTGTG	Query Match  13.0%: Score 120.4; DB 9; Length 149940;  Best Local Similarity 61.5%: Pred. No. 5.1e-19;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 156; Indels 74; Gaps 8;  Matches 368: Conservative 0; Mismatches 161; IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	n BAC	279     <800     2301     2337     655     <800       1323     1307     2753     2805     1341     1323       12     <800     490     <800     1563     1521       2101     2067     177     <800     690     <800       2101     2067     177     <800     690     <800       4290     4236     6836     6740     998     1005       1154     1166     6767     6740     509     <800       1154     1166     6767     6740     509     <800       6886     6882     5959     5684       7307     7318     10600     10609       5616     5684
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Oy 60  Db 2  Oy 12  Db 8  Oy 16  Db 11	BASE COUNT ORIGIN ORIGIN Query Mai Best Loci Matches	. CDS	PUBMED FEATURES	TITLE	AUTHORS TITLE JOURNAL REFERENCE RUTHORS	-	_	Db 79389 TYV Oy 764 TG. Db 79449 TA Oy 820 CA Db 79509 CC
9 GACCGRECTEL SCHOOL STATES OF THE STATES OF	signal 222 a	/clone="N7.2" /clone="N7.2" /clone=lib="lambda gtll cDNA library" /clone_lib="lambda gtll cDNA library" /clone_lib="lambda gtll cDNA library" /locolor="nucleoplasmin" /product="nucleoplasmin" /protein_id="cAA68363.1" /protein_id="GI:833629" /db_xref="SH:833629" /db_xref="SH:83-PROT:P05221" /db_xref="SH:SS-PROT:P05221" /db_xref="SH:SS-PROT:P05221" /clorkARODEFINEIVTOREGKEKEPVPIASLKPSILPMATMVGIELTPPVTFRLKAGS /LIBRARDEFINEIVTOREGKEKEPVPIASLKPSILPMATMVGIELTPPVTFRLKAGS CLGDKARODEFINEIVTOREGKEKEPEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	88112783 3428591 Location/Qu 1: .646 /organism="	pleoplasmin from xenopus laevis oocytes and analymental expression (1987)	bmission  de Robertis E., University of Cal (02-FEB-1987) de Robertis E., University of Cal (02-FEB-1987) de Robertis E., University of Cal I (02-	I GI: lasmir laev laev ta; M ta; Ma; Ba inae;	XLNUPLR 646 bp mRNA linear VRT 10-FEB-1999 Xenopus laevis mRNA fragment for nucleoplasmin.	TICCITIGGCIGTGCTGTGGTCATGGGGTGTACCCCTACCCTTGCCCCTTCCATCTGAGTC 79448  TGAATGCAACAGGGGTGTTGCGGGGGCAACATGAGAGCCCCTCACCCCCAACTCTC 819  TGAATGCAACAGGGGTGTTTTGGAGAAAGTGACAAAAGATCCTCTCTCACTCA



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Best Local
356 AAAGCCTTCTATTCTACCCATGGCAACTATGGTGGGCATTGAGCTGACTCCTCCAGTTAC
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            273 CCAGGCCTCAGTCCTCCCATGGTCTCCATGGTAGGAGTGCAGCTTTCTCCCCCAGTTAC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                           305 AÁTCGTTACACAÁGAGGAGGGAGCÓGAAA-----AATCTGTTCCAÁTTGCCACTCT 355
                                                                 213 GATCCTGCCCCAGCAAACCAGGAGGACAAGAAGATGCAGCCGGTCACCATTGCCTCACT 272
                                                                                        245 GTTGGCGTTGCGCACGGTGTGTCTGGGGGACAAGGCAAAGGATGAGTTCAACATTGTAGA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 CATCAGTGGTCAACACGTAGCAATGGAGGAAGATTACTCATGGGCAGAAGAGGGAAGATGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 CCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAGGAGGAAGA 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 GATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTCCTCCCATGGTCTCCATGGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and signals
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87218476
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Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                              Conservative
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gwall, C., Dilworth, S.M., Black, S.J., Kearsey, S.E., Cox, L.S.
                                                                                                                                                                                                              /note="polyA site"
153 c 222 g
                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:P05221"
/translation="MASTVSNTSKLEKPVSLIWGCELNEODKTFEFKVEDDEEKCEHQ
LALRTVCLGDKAKDEFNIVEIVTQEEGAEKSVPIATLKPSILPMATMVGIELTPPYTF
RLKAGSSPLYISGOHVAMEEDYSWAEEEDEGGAEGEEEEEEEDOESPPKAVKRPAAT
                                                                                                                                                                                                                                                                                                      /protein_id="CAA28460.1"
/db_xref="GI:64940"
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114...716
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                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Zorganism "Xenopus laevis"
                                                                                                                                               10.4%; Score 96.2; DB 5; L 54.9%; Pred. No. 3.4e-13; Live 0; Mismatches 188;
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ORIGIN
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      Matches
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166494/c
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664 AAATGAGGAGCCACGCCTTGGGGGGGCACGGTGCAAAGTGGGCCTTCCCTGGGCTGTGCTG
                                                                                                                                                                                                                                                                                                                                             VERSION
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                                                    JOURNAL
                                                                                   DEFINITION
                                     604 GACAAGAGCCCTGTGAAAAAGGCCAAAGCCCACAGCCAGAGCCAAGAAGCCAGGATTCAAG 663
                                                                                                                                                                                                                                                                                      TITLE
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                                                                   544 AGCGTGGCTAAGAAAAAAAGCTGGAAAAAGAAGAAGAAGAATAAGAGCCAGCGTTAGA 603
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                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                         1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                     Unclassified.
                                                                                                                                                                                                                                                                                                               Unknown
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                                                                                                                                                                                                                                                                                                                                           Sequence 14 from patent US 5670367.
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1491 c 1486 g
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1. .7218
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                                                                                                                                                                                               10.1%; Score 93.2; DB 6
3.5%; Pred No. 2.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 209, Application US/08781891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 609062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 TTCCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            724 CAGGCACAGGGTGCCCCTGTCCAGCCCCTCCACCTG 759
                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFAX: (206) 1D NO: 209:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                        ATTORNEY/AGENT INFORMATION:
ANAB: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
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                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                  CLASSIFICATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                         Washington
                51259 base pairs nucleic acid
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oshima, Junko
                                                                                                                                                                                                                                                                                                               USA
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57; Mismatches 125; Indels
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US-08-781-891-208/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 208,
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                                                                                                                                    US-08-781-891-208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OShima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fu,
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                                                                                Matches
                                                                                                          Query Match
                                                                                           Best Local Similarity
                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenhuro
                        TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                           NAME: NO. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317 REFERENCE/DOCKET NUMBER: 240052.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                    376 CAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAAGAAGAAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
436 GAGGAGGAAGAGGAAGAAGAAGAATGAAGGATGAGGATGCAGAATAATATCTCTGGAGGAG 495
                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                   STRANDEDNESS:
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                                                                                       6.4%; Score 59.4; DB 3; Length 16442; 57.6%; pred. No. 1.1e-05; ative 0; Mismatches 91; Indels 1;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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        January 24, 2003, 05:06:35; Search time 77 Seconds (without alignments) 3680.121 Million cell updates/sec
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      Issued_Patents_NA: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
      DB
  US-08-232-463-14
US-08-781-891-209
US-08-781-891-208
US-08-781-891-208
US-08-728-323A-1
US-09-298-568-1
US-09-298-569A-20
US-08-770-379-20
US-08-770-379-20
US-08-574-959A-6
US-09-357-014-6
US-09-404-959-3
US-08-785-411-3
US-08-785-610-2
US-09-262-610-2
US-09-262-610-2
US-08-459-6858-3
US-08-39-411-3
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1, Appli 20, Appli 8, Appli 8, Appli 8, Appli 8, Appli 9, Appli 19, Appli 19
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US-08-922-635-21	US-08-922-635-1	US-08-650-766-1	US-08-922-635-3	US-08-650-766-3	US-08-741-134-1	US-08-922-635-2	US-08-650-766-2	US-08-374-219B-10	US-07-865-662F-10	US-08-296-362-1	US-09-345-882-1	US-09-345-882-4	US-09-345-882-21	US-09-130-114-2	US-09-249-585A-4	US-09-528-706-3	US-09-586-472-3
21	Sequence 1, Appli	Sequence 1, Appl1	Sequence 3, Appl1	Sequence 3, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	-	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 21, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 3, Appl1	Sequence 3, Appli

#### ALIGNMENTS

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US-08-232-463-14
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 394
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
ADDRESSEE: Foley & Lardner
                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                             TOPOLOGY:
                                                                              STRANDEDNESS:
                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                  TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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ZIP: 22313-0299
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CITY: Alexandria
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Query Match

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                                                               INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                            CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: NO. 6090620tenhuro
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                                            SEQUENCE CHARACTERISTICS:
                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 AAATGAGGAGCCACGCCTTGGGGGGGCACGGTGCAAAGTGGGCCTTCCCTGGGCTGTGCTG 723
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                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              APPLICATION NUMBER: US/OFILING DATE: 27-DEC-1996
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STRANDEDNESS:
                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                             NAME: No. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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        : 51259 base pairs nucleic acid
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                                                                             (206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schellenberg, Gerald D.
/ENTION: GENE AND GENE PRODUCTS RELATED TO
/ENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oshima, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu, Chang-En
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single
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57; Mismatches 125;
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Best Local Similarity
                                                                                        Matches
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                                                                                                                                                                                                                                      TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                              APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fu, APPLICANT: Yu,
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 CAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAAGAAGAAGGGGAG 435
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                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                    Local Similarity
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                        NAME: No. 6090620tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                    16442 base pairs
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                linear
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59.9%;
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57.6%;
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Pred. No. 1.6e-06;
"" matches 71;
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                                                                                        Score 59.4; DB 3;
Pred. No. 1.1e-05;
0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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                                                                                                                  Length 16442;
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                                                                                                                            Matches 151;
                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: MOORE, PA
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                            468 TGAGGATGCAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGT 527
                                                                             COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: S11
TYPE.
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                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                        LENGTH:
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CANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                       3489 base pairs
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                                                                                                                           Conservative
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Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                          single
                                                                                                                                    6.4%; Score 59.2; DB 2; 52.8%; Pred. No. 6.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isidore S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA
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                                                                                                                       Mismatches 133;
                                                                                                                                                 Length 3489;
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RESULT 6
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Best Local Similarity 52.8%;
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Chang, Yuan
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APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RRADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DAYF: 1999-04-21
EARLIER APPLICATION NUMBER: US/60/109,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09298568 Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Boheńźky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT:
                                                                                                                                                                                                                                                                                                                     1101 GGATGACGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGA 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 133; Indels
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20896 GGATGACGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGGA 20837
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                        APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 32207 base present the stranded stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                        Bohenzky, Roy A.
                                                                                                                                                                                                                                                                                                                                                         Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooper & Dunham LLP
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Cooper & Dunham LLP
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52.8%;
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Pred. No. 1.6e-05;
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Matches 151:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                               APPLICANT: Edelman, Isidore S
APPLICANT: MOOTE, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION UNMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1997-07-22 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE:
CLASSTETCT:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 AAGAGCCAGCGTTAGAGACAAGAGCCCTGTGA--AAAAGGCCAAAGCCACAGCCAGAGCC 645
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Bohenzky, Roy A
                                                                                                                                                                                                                                                                                                                                                                                                 Russo, James
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                                                                          PCT/US97/13346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45185-F
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Pred. No. 1.6e-05;
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GENERAL INFORMATION:
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LENGTH: 32207
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
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ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DEN-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20716 GGACGGGGGGGATGGAAACAAAACGTTGAGCATCCAAAGTTCACAACAGCAGCAGGAGCC 2065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20776 TGATGAGGACAATGAGGACGAGGAGGATGACGAGGAGGAGGACAAGAAGGAGGACGAGGA 20717
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: p62 POLYPEPTIDES, TITLE OF INVENTION: AND USES THEREFOR
                   FEATURE:
                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 AAGAGCCAGCGTTAGAGACAAGAGCCCTGTGA--AAAAAGGCCAAAAGCCACAGCCAGAGCC 645
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                                                                                        TYPE: nucleic acid
NAME/KEY:
                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
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nes 151; Conserv
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                                                                                                                                                            (617)227-7400
(617)227-5941
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US-09-357-014-8
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US-09-357-014-8
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Best Local Similarity 57.1%;
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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           SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                               NAME/KEY: CDS
LOCATION: 439.
                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/574,959 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/357,014
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                                                                                                                                                      LENGTH: 3211 base pairs
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             SEQ ID NO:
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Pred. No. 1.6e-05;
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                                                                                            Matches 105;
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2458 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAACTTTGAAGAAGAAGAAGAAGAAGAAGAA 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O:
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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LENGTH: 3901 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 CCCCAGAAGCAGGCGAGCGTGGCTAAGAAAAAAGCTGGAAAAAAGAAGAAGAAGAATA 588
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 AGAG 592
                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polar
 469 GAGGATGCAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTG 528
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                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                              0; Mismatches
                                                                                              Score 57.6; DB 2; Length 3901; Pred. No. 1.7e-05; O; Mismatches 79; Indels 0
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RESULT 12
US-09-357-014-6
US-09-357-014-6
; Sequence 6, Application
; Patent No. 6291645
; GENERAL INFORMATION:
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Best Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                   3148 GAAGAAGAGGAAGAAGAAGAAGAAGAAGAACTTTGAGGAAGAAGAAGAAGATGAAGAG 3207
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529 CCCCAGAAGCAGGCGAGCGTGGCTAAGAAAAAAAGCTGGAAAAAGAAGAAGAAGAAATA 588
                                                                           469 GAGGATGCAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTG 528
                                                                                                                                         COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-Jul-1999 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/357,014
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                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3901 base pairs
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                                                                                                                                                                                                                                                                                                                        439..3847
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                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                     Score 57.6; DB 4; Length 3901; Pred. No. 1.7e-05; O; Mismatches 79; Indels 0
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; LOCATION: (112)..(2235)
US-09-433-699-3
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US-09-433-699-3
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APPLICANT: Yang, Xiaolu

APPLICANT: Khostavi-Far, Roya

APPLICANT: Chang, Howard Y.

APPLICANT: Baltimore, David

TITLE OF INVENTION: DAXX, A NOVEL FAS-BINDING

TITLE OF INVENTION: PROTEIN THAT ACTIVATES JNK
                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
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Best Local Similarity
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SEQ ID NO 3
LENGTH: 2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: LEX M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REFERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
COUNTY: 02210
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09433699B Patent No. 6165786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                        Boston
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                                                                                                                                            600 Atlantic Avenue
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)...(2338)
US-09-490-692-3
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                                                                                                                       SEQ ID NO 3
LENGTH: 2477
                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09490692 Patent No. 6180353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%;
Best Local Similarity 55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 108;
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/490,692 CURRENT FILING DATE: 2000-01-24
                                                                                                                                                                                                                             APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTS-0120
                                                                                                                                                                   NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4:
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APPLICATION NUMBER: 60/0
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 AGACAAGAGCCCTGTG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 GAGCGTGGCTAAGAAAAAAGCTGGAAAAAGAAGAAGAAGAAATAAGAGCCAGCGTTAG 602
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REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: M0656/7036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/0 FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/022,983
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Pred. No. 5.7e-05;
0; Mismatches 88; Indels 0
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GenCore version 5.1.3 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database : Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Sequence: Title: Perfect score: OM nucleic - nucleic search, using sw model Searched: Scoring table: Run on: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 January 23, 2003, 14:06:24 ; Search time 45576 Seconds (without alignments) 590.025 Million cell updates/sec 2054640 seqs, 14551402878 residues US-09-844-864-16 924 1 cagcccgcttctctgcccgg.....tttgcggccgcaagcttatg 924 : gb\_om:\*
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

AUTHORS	סקקקטקארק קארקקקארק	ORGANISM	SOURCE	VERSION KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1 AK094267
Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Clone: BRACE2005719. Homo sapiens	Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2	AK094267.1 GI:21753294	to NUCLEOPLASMIN. AK094267	AK094267 1874 bp mrna linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ36948 fis, clone BRACE2005719, weakly similar	

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JOURNAL
REFERENCE
AUTHORS
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/note="cloning vector: pME18SFL3"
/note=570 c 604 g 306 t
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/clone="BRACE2005719"
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                                                                                            AGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGATTTGCTTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 410 from Patent WO0172295. AX321879
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                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., MacLean, C., McCarthy, M., Marquis, N., Matthews, C., McCarthy, M., McBhean, C., McCarthy, M., McBhean, P., McKernan, K., McPheeters, R., Maldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Swyar, P., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Travers, M., Travis, N., Trajilio, J., Vassillev, H., Vlal, R., Vo, A., Wilson, B., W., X., Wyman, D., Ye, W.J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### HITTH | HI
Submitted (23-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2002 this sequence version replaced gi:22123594. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 156347)
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                 Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROGRESS ***,
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AC023288
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Query Match 28.4%;
Best Local Similarity 99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87028 TTGGGGGGCACGGTGCAAAGTGGGCCTTCCCTGGGCTGCTGCTGCAGGCACAGGGTGCCCC 87087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                            861 CACAATAAAGTTGCCTGGTCAGGA 884
                                                                                                                                                                                                                                                                                                                                                                                      801 CCCCTCACCCCCAACTCTCCACTTTCAGGAGGCCCCCAGTGAAGAGCCCCCACCTCGGGGT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 TTGGGGGGCACGGTGCAAAGTGGGCCTTCCCCTGGGCTGTGCTGCAGGCACAGGGTGCCCC 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 AAAGGCCAAAGCCACAGCCAGAGCCAAGAAGCCAGGATTCAAGAAATGAGGAGCCACGCC 680
                                                                                                                                                                                              CACAATAAAGTTGCCTGGTCAGGA 87231
                                                                                                                                                                                                                                                                                                                         CCCCTCACCCCAACTCTCCACTTTCAGGAGGCCCCCAGTGAAGAGCCCCACCTCGGGGT 87207
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCCAGCCCTCCACCTGTGTCTGAATGCAACAGGGGTGTTGCGGGGGGCAACATGAGAG
   Homo sapiens chromosome 8
                              AC023288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 44565: contig of 44565 bp in length
44566 44665: gap of 100 bp
44666 99572: contig of 54907 bp in length
99573 99672: gap of 100 bp
99573 104441: gap of 100 bp
104442 104441: gap of 100 bp
104442 123153: contig of 18712 bp in length
123154 123253: gap of 100 bp
123254 137735: contig of 14882 bp in length
13736 137835: gap of 100 bp
137836 156347: contig of 18512 bp in length
123254 137735: contig of 18512 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC" 39805 a 37308 c 37797 g 40934 t 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L12352
Center clone name: 67_H_12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-67H12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 262.4; DB 2; Length 156347; Pred. No. 3.2e-54;
                                  166878 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
clone RP11-67H12, WORKING DRAFT SEQUENCE,
                                  DNA
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                                  linear
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                           HTG 22-FEB-2001
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0,

AC023288

15 unordered

pieces.

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JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry, Dye terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 151238 bases at least Q40
Consensus quality: 155909 bases at least Q30
Consensus quality: 157935 bases at least Q30
Consensus quality: 157935 bases at least Q30
Consensus quality: 157935 bases at least Q20
Insert size: 16447; sum-of-contigs
Insert size: 165478; sum-of-contigs
Quality coverage: 9.4x in Q20 bases; sum-of-contigs
Quality coverage: 6.6x in Q20 bases; sum-of-contigs.
** NOTE: This is a 'working draft' sequence. It currently
** consists of 15 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M. Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J., Yu,S., and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-FEB-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu, S. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmalia; Eutheria; Pr
(bases 1 to 166878)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
Sequencing Vector: M13mp18; X02513
Sequencing Dye-reimer: 0% of reads
Chemistry: Dye-terminator Big Dye:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: 836
Center clone name: RP11-67H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://sequence-www.stanford.edu/group/human/Contact: hum-info@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
26031
26131
33533
33633
46268
46368
61797
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10645
10745
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2276
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  61896:
                                                                                                                                          26030:
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g of 8244
                                                                                                                                                                                                                     f unknown
y of 2181
f unknown
of 2629
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g of 1774
                                                                                                                                                                                unknown
of 4213
                of 12635 bp in length
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of 15429 bp in length
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QΥ
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                                                                                                                                                                    Db 146814 TTGGGGGCACGGTGCAAAGTGGGCCTTCCCTGGGCTGCTGCTGCAGGCACAGGGTGCCCC
                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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Best Local Similarity
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                               misc_feature
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4573. .6489
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17787. .26030
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2276. .4472
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig41"
132788. .166878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI human BAC library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig39"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig28"
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78616: gap of unknown length
97532: contig of 18916 bp in length
97632: gap of unknown length
132687: contig of 35055 bp in length
132787: gap of unknown length
132787: gap of unknown length
166878: contig of 34091 bp in length.
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Pred. No. 3.2e-54;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              1413 others
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0,

Db 146994 CACAATAAAGTTGCCTGGTCAGGA 147017

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ACCESSION
VERSION
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AC090442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-FEB-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Jun 13, 2001 this sequence version replaced gi:13112136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 181714)

Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Lehmann, R., Menzel, U., Polley, A., Schilhabel, M.B., Schudy, A., Siddiqui, R., Taudlen, S., Wen, G., Rosenthal, A. and Platzer, M. Chromosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center Jena.
Direct Submission
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Homo sapiens chromosome 8 clone RP11-868P18, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality 10. quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NC090442.2 GI:14389319
                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H522
Center clone name: RP11-868P18
Center clone name: RP11-868P18
Center clone name: RP11-868P18
Sequencing vector: M13; 100% of reads
Sequencing vector: M13; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 167442 bases at least Q40
Consensus quality: 173337 bases at least Q30
Consensus quality: 179477 bases at least Q20
Quality coverage: 5.19 x in Q20 bases; sum-of-contigs
                                                            3437
3537
10121
10221
12192
12192
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22795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: gscj-submit@genome.imb-jena.de
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                                                                                    3436: contig of 3436 bp in length 3536: gap of unknown length 10120: contig of 6584 bp in length 10220: gap of unknown length 12191: contig of 1971 bp in length 12291: gap of unknown length 22694: contig of 10403 bp in length 22694: gap of unknown length
                                                                                                            gap of unknown length contig of 10403 bp in length
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unknown length
of 1121 bp in length
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В
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                                      ORGANISM
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                                                                  ACO87819.2 GI:13194968
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                    Homo sapiens
                                                                                                                          SEQUENCE,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                           Homo sapiens chromosome 8 clone RP11-507M15
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76239
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//note="Please note that a sequence read was obtained using vectorprimers. This read represents the right end of the clone. However, within this read, the cloning site, e.g. the exact end of insert could not be identified.'"
a 40820 c 40243 g 51096 t 1400 others
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/db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                          20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-868P18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117474: gap of unknown length
163683: contig of 46209 bp in
163783: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181714: contig of 17931 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105935: gap of unknown length 117374: contig of 11439 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43916:
60529:
60629:
66757:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of unknown length contig of 12182 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 4721 bp in length gap of unknown length
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contig of 16613 bp in length
gap of unknown length
contig of 6128 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 262.4; DB 2; Pred. No. 3.2e-54;
                                                                                                                                                              184050 bp
                                                                                                                                         linear
5 map 8,
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WORKING DRAFT
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Trayls, N., Triglio, J., Vassilev, H., Viel, R., Vo, A., Willen, P., Viene, T., Vo, A., Willen, R., Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S Barna,M., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,S., Farreira,P., FitzHugh,W., Gage,D., Galagan,J., Bodge,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Tehoryky, T. Tevino,R., Tin G. Marchan,G. Marchanld,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 8, clone RP11-507M15 Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 4, 2001 this sequence version replaced gi:12584317. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence % \left( 1\right) =1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 184050)
                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 175465 bases at least 040 Consensus quality: 179683 bases at least 020 Consensus quality: 181216 bases at least 020 Consensus quality: 181216 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7.1 in Q20 bases; Quality coverage: 6.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L11344
Center clone name: 507_M_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 170000; agarose-fp
Insert size: 182150; sum-of-contigs
                                                                                                                                                                                                               29338: contig of 29338 bp in length
29339 29438: gap of 100 bp
29439 29457: contig of 19 bp in length
29458 29557: gap of 100 bp
29558 30186: contig of 629 bp in length
                                                                                                                                                             30187 30286: gap of 100 bp
30287 31083: contig of 797 bp in length
                                                                      31979
                                                                                                                                  31084 31183:
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31183: gap of 100 bp
31978: contig of 795 bp in length
32078: gap of 100 bp
32748: contig of 670 bp in length
32848: gap of 100 bp
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93274 101147: contig of 7774 bp in length

101048 101147: gap of 100 bp

101148 111284: contig of 10137 bp in length

111285 111384: gap of 100 bp

111285 130797: contig of 19413 bp in length

130798 130897: gap of 100 bp

130898 155534: contig of 21637 bp in length
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182986 184050; contig of 1065
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88674 93173: contig of 4500 bp in length
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34031 34130:
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29558. 30186
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72508. .75697
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30287. .31083
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                                                                                                           /note="assembly_fragment"
111385. .130797
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82251. .88573
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35258. .72407
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          /note="assembly_fragment"
                                              130898
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250: gap of 100 bp
250: gap of 100 bp
88573: contig of 3942 bp in length
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130: gap of 100 bp
35157: contig of 1027 bp in length
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                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Perreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-elerre, N., Hagos, B., Heaford, A., Horton, L., Hulne, W., Illey, I., Johnson, R., Jones, C., Karatas, A., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Mar, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., Lamazares, R., Landers, T., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Polnetis, R., Naylor, J., Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tevals, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M.
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es 263; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Pred. No. 3.2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2001 this sequence version replaced 91:14196391. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 868 p 18

Center clone name: 868 p 18

Center clone name: 868 p 18

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 180698 bases at least Q40
Consensus quality: 180469 bases at least Q30
Consensus quality: 183469 bases at least Q20
Insert size: 183000; agarose-fp
Ouality coverage: 15.1 in Q20 bases; agarose-fp
Quality coverage: 15.1 in Q20 bases; sum-of-contigs
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105469 133826: contig of 28358 bp in length
133827 133926: gap of 100 bp
130927 170402: contig of 36476 bp in length
170403 170502: gap of 100 bp
170503 184444: contig of 13942 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41746 41845: gap of 100 bp
41846 52788: contig of 10943 bp in length
52789 52888: gap of 100 bp
52889 68506: contig of 15618 bp in length
68507 68606: gap of 100 bp
68607 105368: contig of 36762 bp in length
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24647 24746: gap of 100 bp
24747 28060: contig of 3314 bp in length
28061 28160: gap of 100 bp
28161 33796: contig of 5636 bp in length
33797 33896: gap of 100 bp
33797 41745: contig of 7849 bp in length
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HS833B7
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HS83B7
HUMAN DNA Sequence from clone CTA-833B7 on chromosome 22q12.3-13.2
Contains the NCP4 gene for cytosolic neutrophil factor 4 (40kD), the 5 part of the CSF2RB gene for granulocyte-macrophage
the 5 the CSF2RB gene for granulocyte-macrophage
low-affinity colony stimulating factor 2 receptor beta, ESTs, STSs
                                                                                                                                                                                                                                                                                                        Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerrequest@sanger.ac.uk

On May 18, 1998 this sequence version replaced gi:2578146.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats to the control of 
                                      This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                      annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and GSSs, complete sequence
http://www.sanger.ac.uk/HGP/Chr22
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Em. EMBL, Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between neighbouring submissions. The true right end of clone CITF22-24E5 is at 100 in this sequence The start of this sequence overlaps with sequence 282185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone CTA-833B7 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap
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6873. .7196
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/note="MIR repeat: matches 158. .262 of consensus" 8152. .8228
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/note="MLT1J repeat: matches 1. .261 of consensus"
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                                                                                                  /note="12 repeat: matches 2602. .2750 of consensus"
7347. .7532
                                                                                                                                                                                                                                                                          /note="156 copies 2 mer tg 67 conserved"
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                                                                  /note="MIR repeat: matches 2. .191 of consensus"
                                                                                                                                                                                                                          /note="22 copies 14 mer 67 conserved"
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                                               16065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPQGNSVDRMAAPRAEALEDETGNSKLELNFKAGDVIFLLSRINKDWLEGTVRGATGI
FPLSFVKILKDFPEEDDPTNWLRCYYYEDTISTIKDIAVEEDLSSTPLLKDLLELTRR
EFQREDIALNYRDAEGDLVRLLSDEDVALMVRQARGLPSQKRLFPWKLHITQKDNYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:060808"
/translation="MAVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVFVIE
/translation="MAVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVFVIE
/KTKGGSKYLIYRRYRQFHALQSKLEERFGPDSKSSALACTLPTLPAKVYVGVKQEIA
VKTKGGSKYLIYRRYRQFHALQSKLEERFGPDSKSSALACTLPTLPRTRKVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: cDNAs: Em:AB002665 Em:X77094 Em:U59488; match:-ESTs: Em:AA17839 Em:A1007048 Em:AA465462 Em:AA465389 Em:AA465518 Em:A381340 Em:AA44805 Em:AA975113 Em:AA969460 Em:AA948430 Em:A1435296 Em:A1299103 Em:AA648472 Em:AA702857 Em:A1088359 Em:D20144 Em:AA909156 Em:AA688071 Em:W95229 Em:A1088359 Em:D20144
/note="19 copies 2 mer tt 81 conserved"
16171. ,16218
                                                                                                                                                                                                        14545
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 20. .136 of consensus" 12944. .13247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               notee "match: STS: Em:X77094"

join(12542. 12573,15415. 115499,16289. 16442,18762. 1

21785. 21912,33022. 23079,23697. 23795,27023. 27153,

27399. 27464,28998. 29193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 184. .260 of consensus" 8253. .8341
                                                              'note⇒"MER20 repeat: matches 1. .218 of consensus'
                                                                                                       /note="3 copies 32 mer 95 conserved"
                                                                                                                                              note="L2 repeat: matches 2638. .2710 of
                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 2701. .2741 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L2 repeat: matches 2425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA15486.1"
/db_xref="GI:3136001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="bK833B7.1 (neutrophil cytosolic factor 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L2 repeat: matches 2356. .2502 of consensus"
join(12483. .12573,15415. .15499,16289. .16442,18762. .1
21785. .21912,23022. .23079,23697. .23795,27023. .27464,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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21785 .21912,23022 .23079,23697 .23795,27023 .27153,
27399 .27464,28998 .29288)
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/note="L2_repeat: matches 2164. .2749 of consensus"
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                                               16102
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                                                                                                                                                                                       repeat: matches 2213.
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                                                                                                                                                                                                                                                                       .2728 of consensus'
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Query Match
15893 AGGGGTGTTGTGGGGGCAACACTAAAGTCCCTCACCCCGACTCTCCAGGTGGAGG 15838
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                                                                                                                                                                                                                                                                                                 TAGTGTTAGAGGCCAAGAGCCCCTTGGAAATAGGCCAAACACACATTCAGGCC------ 15998
                                               AGGGGTGTTGCGGGGGCAACATGAGAGCCCCCTCACCCCCAACTCTCCACTTTCAGG 829
                                                                                                 GGCTGTGCTGTGGGTGCAGGATGC------CCCCTCCATCTGTGTCTGAATATGAC
                                                                                                                                   GGCTGTGCTGCAGGCACAGGGTGCCCCTGTCCAGCCCTCCACCTGTGTGTCTGAATGCAAC 773
                                                                                                                                                                                                                                                                                                                                                                                                  TGGCTAAGAAAAAAAGCTGGAAAAAGAAGA------AGAGGAAATAAGAGC
                                                                                                                                                                                                  -----CAAGAAATGAGGAGCCATGCCTTGGAGGTCATGGTGCAGAGTGAACCTGCCCCT 15944
                                                                                                                                                                                                                            AGGATTCAAGAAATGAGGAGCCACGCCTTGGGGGGGCACGGTGCAAAGTGGGCCTTCCCCTG 713
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20478. .20578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ499165"
19252. .19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2638. .2702 of consensus" complement(18442. .18745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18193. .18242
/note="L2 repeat: matches 2702. .2750 of consensus"
18243. .18412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16173. .16214
/note="7 copies 6 mer tcctcc 81 conserved"
17561. .17987
/note="L2 repeat: matches 1251. .1706 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="16 copies 3 mer cct 77 conserved" 16173. .16214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 9. .104 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="3 copies 12 mer 94 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: STS: Em:HSA0462A5; match: STS: Em:Z51609"
18481. .18516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER5B repeat: matches 1. .175 of consensus"
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Pred. No. 9.8e-32;
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COMMENT
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-JAN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence {\sf N}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It current.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye; 80% of reads Assembly program: Phrap; version 0.990319 consensus quality: 131485 bases at least 040 consensus quality: 133037 bases at least 030 consensus quality: 133846 bases at least 020 consensus quality: 133846 bases at least 020 reserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 180200; 27.0% error; agarose-fp
Insert size: 134306; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; agarose-fp
Quality coverage: 10.2x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: RP11-114C6 (bc0623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator ET; 20% of reads Chemistry: Dye-terminator Big Dye; 80% of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; 100% of reads
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                                      /note="assembly_name:Contig18" 39162. 46549
                                                                                                                                                                   /note="assembly_name:Contig15"
11111. .18451
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                       /clone="RP11-114C6"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                           /note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                   /clone_lib="RPCI human BAC library 11"
                   note="assembly_name:Contig19"
                                                                                                    /note="assembly_name:Contig17"
                                                                                                                                           note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                              79227: gap of unknown length
99937: contig of 20710 bp in length
100037: gap of unknown length
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79127:
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                                                                                                                                                                                                              .11010
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                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 149940) Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                       Homo sapiens chromosome 3
AC093557 AC022225
AC093557.3 GI:19698701
2 (bases 1 to 149940)
Kaul, R.K., Olson, M.V.,
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   Raymond, C., Clendenning, J., Ivey, R.G. and
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	TITLE JOURNAL	TITLE JOURNAL REFERENCE
Center: University of Washington Genome Center Center Code: UNGC. Center Code: UNGC. Center Code: UNGC. Contact: university of Washington Genome Center Center Code: UNGC. Center Clone name: RP11-5622 (bc0176)  Sequencing vector: plasmid: 108752; 0% of reads Sequence vector: plasmid:	Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D. Direct Submission Submitted (24-MAR-2002) Genome Center, University of Washi Box 352145, Seattle, WA 98195, USA	Haugen,E.D. Direct Submission Submitted (01-SEP-2001) Genome Center, University of Washi Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 149940) Kaul B K (1605)
Center: University of Was Center: University of Was Center: Ode: UNGC Web site: http://www.geno Contact: ungchtgs@u.washi Drafting Center: BCM Web site: http://www.geno Contact: ungchtgs@u.washi Drafting Center: BCM Web site: http://www.geno Contact: ungchtgs@u.washi Drafting Center: BCM Center project name: Chr- center project name: Plasmi Sequencing vector: plasmi Consensus quality: 149340 Consensus quality: 149340 Consensus quality: 149340 Consensus quality: 149340 Consensus quality: 149940; sum- lapping Sequences: Sequence Ouality Assessment: Sequence Ouality Assessment: Sequence was finished as entry has been annotate. Inty levels above 40 are annotate. Interest plasmi Levels above 40 are annotat	ssion ssion 4-MAR-2002 Seattle, W	ssion 1-SEP-2001 Seattle, W to 149940)
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AGGGTGCCCCTG	CGCCTT      AGAGAGGGCCTG	GAGCCAAGAAGC 	AGGAAATAAGAG    GATTGAGA	GCTGGTGCCCC          GTGGGGGACCCA	ATGAGGATGAGG	TAACCTGGGAGG             TAACCTGGGAAG	CCGGGCTGGCT	Score 120.4; Pred. No. 5.1e 0; Mismatches	Homo sapiens" aaxon:9606" ="3" 1-56P22" *"RPCI human BAC	4176		4421		506	5616	1060	595	559	676	683	ш.	490	27	23
- 1	GGGGGGCA           TGAGACCA	CAGGATTC          CAGGTTCC	CCAGCGTT	AGAAGCAG          AGAAGCTG	ATGCAGAT	AGGAGGAG          AGGAAGAA	CAGGACCO          CCAAATCO	DB 9; le-19; s 156;	C library	4156	1892	4433	<800	5054	5684	10609	5945	5684	6740	6740	<800	<800	2805	2337
AGCCCCTCCACCTGTGTC	GCCTTGGGGGGCACGGTGCAAAGTGGGCC	TGAAAAAGGCCAAAGCCACAGCCAGAGCCAAGAAGCCAGGATTCAAGAAATGAGGAGCCA   TGAGAAAGAACAAACCCATACTCAAACCTAAGAAACCAGGTTCCAAGAAATAAGGAGCCA	AAAAAAAGCTGGAAAAAGAAGAAGAAGAAGAAATAAGAGCCAGCGTTAGAGACAAGAGCCCTG	AAAGCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAGGCGAGCGTGGCTAAGA 	AGGAGGAAGAGGAAGAGGAAGATGATGAGGATGAGGATGCAGATATATCTCTGGAAGGAGC 	AGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAAGAAGAAGGAGGGGAGG 	TITCTCCCCAGITACITTCCAGCTCCGGGCTGGCTCAGGACCCGIGTTCCTCAGIGGCC	Length 149940; Indels 74; 0	y 11"										50	! ! ! !	69	156	134	65
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                                  186 AGCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAACCAGGAGGACAAGAA 245
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                                                                                                                                                                                  69
                                                                      89 AGACGAGGAAGAAAATGTGAGCATCAGTTGGCACTGCGCACAGTATGTCTTGGGGACAA 148
                                                                                                                                          29 GTCCCTTATTTGGGGGTGTGAACT&AATGAGCAGAACAAGACATTTGCGTTTAAAATAGA 88
                                                                                                                                                                                GGCAAAGGATGAGTTCCACATAGTAGAAAT----
                                                                                                        GCTGGAGGGGAAGCAGAGCTGCAGGCTGTTG----CTTCATACGATTTGCTTGGGGGAGAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis mRNA fragment for nucleoplasmin. Y00204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-FEB-1987) de Robertis E., University of California, Dept. of Biological Chemistry, University of California, Los Angeles, CA 90024, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaing of nucleoplasmin from Xenopus laevis oocytes and analysis of its developmental expression Genes Dev. 1 (1), 97-107 (1987)
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Burglin, T.R., Mattaj, I.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Robertis, E.
Direct Submission
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Xenopus laevis
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                 /translation="ntskvekpyslimgcelneqnktfafkiedeeekcehqlalktv
CLGDKAKDEFHIVEIVTQEEGKEKPVPIASLKPSILPMATMVGIELTPPVTFRLKAGS
GPVYISGQHVAMEEDYSWAEEEDEGEEEEEEEDPESPPKAVKRPAATKKAGQAKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=3
/product="nucleoplasmin"
/protein_id="CAA68363.1"
/db_xref="GI:833629"
/db_xref="SWISS-PROT:P05221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="N7.2"
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Pred. No. 4.8e-14;
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                                                                                    GATCCTGCCCCAGCAAACCAGGAGGAGAAGAAGATGCAGCCGGTCACCATTGCCTCACT
AAAGCCTTCTATTCTACCCATGGCAACTATGGTGGGCATTGAGCTGACTCCTCCAGTTAC
                             CCAGGCCTCAGTCCCCCATGGTCTCCATGGTAGGAGTGCAGCTTTCTCCCCCCAGTTAC
                                                                                                                                 GTTGGCGTTGCGCACGGTGTGTCTGGGGGACAAGGCAAAGGATGAGTTCAACATTGTAGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCAGTGGTCAACACGTAGCAATGGAGGAAGATTACTCATGGGCAGAAGAGGAAGATGA
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Xenopus laevis
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Dingwall, C., Dilworth, S.M.,
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LALRTVCLGDKAKDEENIVEIVTQEEGAEKSVPIATLKPSILPMATMVGIELTPPVTF
                                                                                                                                                                                                                                                                                                                                    KKAGQAKKKKLDKEDESSEEDSPTKKGKGAGRGRKPAAKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA28460.1"
/db_xref="GI:64940"
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54.9%;
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Pred. No. 3.4e-13;
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                       664 AAATGAGGAGCCACGCCTTGGGGGGCCACGGTGCAAAGTGGGCCTTCCCCTGGGCTGTGCTG
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                                                                                                    AGCGTGGCTAAGAAAAAAAGCTGGAAAAAGAAGAAGAAGAATAAGAGCCAGCGTTAGA 603
                                                                                                                                                       AGAAGAAGAAGAAATAAGAGCCAGCGTTAGAGACAAGAGCCCTGTGAAAAAAGGCCAAAGC
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166494
                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 186437 bases at least Q40
Consensus quality: 19477 bases at least Q20
Consensus quality: 191697 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 4.53 in Q20 bases; agarose-fp Quality coverage: 4.25 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: M_BA0322K01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 198421)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 203000; agarose-fp
Insert size: 196692; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                  as soon as it is available and be preserved.
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30 unordered pieces.
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4437. .5587
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21754. .23575
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8517. .10353
                                                                                                                                                                                                                                             /note="assembly_name:Contig33" 7010. .8416
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10000"
/chromosome="UNK"
/clone="RP23-322K1"
   /note="assembly_name:Contig40"
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 190604)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                Mus musculus chromosome UNK clone RP23-279L13, WORKING DRAFT SEQUENCE, 17 unordered pieces.
                           Unpublished
                                                                                                                                 Mus musculus
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HTG; HTGS_PHASE1; HTGS_I
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198095. .198421
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123928. .138453
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TITLE
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                                                     source
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184891 bases at least Q40
Consensus quality: 186045 bases at least Q30
Consensus quality: 186920 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 189444; sum-of-contigs
Quality coverage: 6.43 in Q20 bases; sum-of-contigs
Quality coverage: 6.43 in Q20 bases; sum-of-contigs
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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            /organism="Mus musculus"
/db_xref="taxon:10090"
                                                     1. .190604
/chromosome="UNK"
                                                                    Location/Qualifiers
                                                                           68607: gap of unknown length
84968: contig of 16361 bp in length
85068: gap of unknown length
116294: contig of 31226 bp in length
116394: gap of unknown length
190604: contig of 74210 bp in length
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/note="assembly_name:Contig24"
/note="3588.9782
/note="45555"
/note="45555"
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1762. 3532
/note="assembly_name:Contig22
clone_end:SP6
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29000. .35723
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/note="assembly_name:Contig31"
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GenCore version 5.1.3 Compugen Ltd.

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2: //SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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ABL33033 ABI99537 AAS68925 ABA63148		AAK67071 AAS90676 ABQ54697 AAS68926 AAS68538
n im e is enco	Human Immune/haema DNA encoding novel Human breast cell Human breast cell Human bone marrow Probe #13879 for g Human bone marrow Probe #1332 used Probe #1332 used Probe #8947 used t Human breast cell Human breast cell Human breast cell Human bone marrow Probe #3972 for ge Human bone marrow Probe #3972 for ge Human bone marrow Probe #4038 for ge Probe #4038 for ge Probe #4172 used t Probe #394 used t Human genome-deriv Partial mouse WRN	Human immune/haema DNA encoding novel Human ovarian anti DNA encoding novel DNA encoding novel

#### ALIGNMENTS

RESULT 1 AAA72432 Human nucleic acid-binding protein NuABP-51 cDNA. 19-DEC-2000 (first entry) AAA72432 standard; cDNA; 1048 AAA72432; ВP

Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST; expressed sequence tag; drug screening; recombinant expression; antibody; reproductive disorder; infertility; immunological disorder; neurological disorder; cell proliferative disorder; cancer; tumour; ss.

Homo sapiens.

W0200044900-A2 03-AUG-2000

28-JAN-2000; 2000WO-US02237

29-JAN-1999; 29-JAN-1999; 99US-0117904 99US-0117905

(INCY-) INCYTE PHARM INC.

Tang YT, Tran B, , Lal P, Hillman JL, Shih LL, Au-Young J Au-Young JL; Yue Azimzai Y, Lu AMD, Baughn MR;

WPI; 2000-499332/44.

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Chascociated with overexpression or underexpression of an analysis and antagonists or and nucleotive, immunological, neurological and cell proliferative disorders. Reproductive disorders chat may be treated using compositions of the invention include confertility, endometriosis, disruptions of the menstrual cycle and confertility endometriosis. Immunological disorders that may be treated include AIDS, allergies, and autoimmune disorders such as complete sclerosis, rheumatoid arthritis, diabetes and systemic lupus crythematosus. Neurological disorders that may be treated include erythematosus. Neurological disorders that may be treated include cand mental disorders such as schizophrenia. Cell proliferative disorders that may be treated include a wide variety of cancers, and also cateriosis at heace of the confers of the concers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a human NuABP nucleic acid, recombinant production of the human NuABPs, and antibodies against the human NuABPs, and also to methods of screening modulators of human NuABP activity or expression. The human NuABPs, and their agonists and antagonists are used to treat diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were produced by extension from an appropriate EST (expressed sequence tag) using primers designed using the EST. The invention also relates to expression constructs, host cells and transgenic organisms comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid binding proteins, used to identify agonists and antagonists of them, for the treatment of reproductive, immunologic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arteriosclerosis, atherosclerosis, cirrhosis and psoriasis.
                         481 ATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAG
                                                                                         421 GAAGAAGAAGGGGAGGAGGAAGAAGAGGAAGATGATGAGGATGAGGATGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAGAAAGCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAACCAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 CAGCCCGCTTCTCTGCCCGGAGCCATGAATCTCAGTAGCGCCAGTAGCACGGAGGAAAAG
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                                                                                                                                                                                                                                                                                                                                GAAGAAGAAGGGGAGGAAGAAGAAGAAGAAGATGATGAGGATGAGGATGCAGAT
                                                                                                                                                     GTGTT&CTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAG
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58; Conservative
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100.0%; Pred. No. 3
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                                                 \rm O1\text{-}180,\ O1\text{-}184 and \rm O1\text{-}236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner –
                                                                                                                                                                                                                                                                                                                                                                                                      Snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse oocyte-specific 01-236 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD00296 standard; cDNA; 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018
                         Claim 22; Fig 5; 54pp; English.
                                                                                                                                                                                                                              28-OCT-1999;
                                                                                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 screen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2000 (first entry)
                                                                                                        P-PSDB; AAY70950.
                                                                                                                      WPI; 2000-350684/30.
                                                                                                                                            Matzuk MM, Wang P;
                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                   28-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 modulator; ss.
                                                                                                                                                                                                    98US-0106020
                                                                                                                                                                                                                              99WO-US25209
                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Mouse oocyte-specific protein, 01-236"
/prote= "Identical to mouse Npm2 protein with the
exception of one residue"
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
156..779
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The present sequence

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the mouse oocyte-specific

gene Npm2, complete

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1019 BP; 334 A; 243 C; 265 G; 177 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynaecological cancers.
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                                            GCTGTGCTGCAGGCACAGGGTGCCCCTGTCCAGCCCCTCCACCTGTGTCTGAATGCAACA 774
                                                                                            GTGACCAAGAAATGA--CCTCATCTTAGCATCTTCTGCGTCCAAGGCAGGATGTCCAGCA
                                                                                                                                         GGATTCAAGAAATGAGGAGCCACGCCTTGGGGGGGCACGGTGCAAAGTGGGCCTTCCCTGG
                                                                                                                                                                                        AGCCCTCAGGACAAGAGTCCCTGGAAGAAGGAAGAATCTACACCCAGAGCAAAGAAGCCA
                                                                                                                                                                                                                                                                                       ATGAGCATAGCAAAGAAAAGAAGGTGGAAAAAGAAGAGGATGAAACAGTAGTGAGGCCC
                                                                                                                                                                                                                                                                                                                                    GCGAGCGTGGCTAAGAAAAAAAGCTGGAAAAAGAAGAAGAAGAAA-----TAAGAGCC 594
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                                                                                                                                                                                                                                        AGCGTTAGAGACAAGAGCCCTGTGAAAAAGGCCAAAGCCACAGCCAGAGCCAAGAAGCCA
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66.48;
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Pred. No. 1.
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1 CAGCCCGCTTCTCTGCCCGGAGCCATGAATCTCAGTAGCGCCAGTAGCACGGAGGAAAAG 60 CAGCCCGCTTCTCTGCCCGGAGCCATGAATCTCAGTAGCGCCCAGTAGCACGGAGGAAAAG 146

Matches

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                              their corresponding cDNA molecules. Lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is a cDNA encoding human lung tumour-specific protein.
Sequence 423 BP; 84 A; 138 C; 125 G; 76 T; 0 other;
                                                                                                                                     The invention relates to isolated lung tumour-specific
                                                                                                                                                                     Claim 1; Page 302; 378pp; English.
                                                                                                                                                                                                                                                                                          Reed
                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000;
05-JUN-2000;
                         is a cDNA encoding human lung tumour-specific protein.
                                                                                                                                                                                              New human lung-specific polynucleotides and polypeptides diagnosis and treatment of disease e.g. lung cancer - {\sf cancer}
                                                                                                                                                                                                                                             WPI; 2001-639201/73.
                                                                                                                                                                                                                                                                                                                                                                          18-AUG-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer; 54589.1; ss.
                                                                                                                                                                                                                                                                          Henderson RA,
                                                                                                                                                                                                                                                                                                                                                              01-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lung tumour-specific 54589.1 cDNA.
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                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                         Lodes MJ,
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2000US-234517P.
2000US-0704512.
2000US-0738973.
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PA, Elliot M,
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        (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte activation; chronic inflammation; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel dis Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA differentially expressed in granulocytic cells #131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK83560 standard; cDNA; 86574 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2000; 2000US-237189P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001WO-US30821.
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                                                                                                                                                                                                                         Claim 1; SEQ ID No 131; 114pp; English.
                                                                                                                                                                                                                                                                                      of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                       Detecting granulocyte activation by detecting differential expression
                                                                                                                                                                                                                                                                                                                                                                                                           Beazer-Barclay Y, Weissman SM,
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                                                                                                                                                                                                                                                                 drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                                   invention relates to detecting (M1) granulocyte (GC) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAAAGCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAACCAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGTGACGACCGTGCTCTGGGGCTGCGAGCTCAGTCAGGAGAGGCGGACTTGGACCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAAGATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTCCTCCCCATGGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAAAGCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAACCAGGAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGTGACGACCGTGCTCTGGGGCTGCGAGCTCAGTCAGGAGAGGCGGACTTGGACCTTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTAGGAGTGCAGCTTTCTCCCCCAGTTACTTTCC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAGATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTCCTCCCCATGGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGATTTGCTTGGGG
                                                                                                                                                                                                                                                                                                                                                                     2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                             Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326
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05-SEP-2000

(first entry)

Oocyte-specific;

ovary; Npm2; nucleoplasmin; mouse; mammalian ortholog;

Mouse ovary-specific Npm2 gene.

AAD00297 standard; DNA;

1481

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cc gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the clevel of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen core sterile inflammatory disease, by contacting a tissue having crimens in the tissue. M1 is useful for detecting GCA; M2 is useful for core modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for cresponse in a subject, exposure of a subject to a pathogen or sterile criminatory disease (e.g. psoriasis, rheumatoid arthritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, creating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes.

CC Inflammatory disease, also bacterial infection, viral infection and M5 is sequence represents a gene differentially expressed in granulocytes.

CC On the printed specification but was obtained in alcorrance.
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 AAGGGGAGGAGGAAGAAGAAGAAGAAGATGATGAGGATGAGGATGCAGATATATCTC 487
                                                                                                                                                                                                                                                                                                        594 CAGCGTTAGAGAGAGAGGCCTGTGAAAAAGGCCAAAGCCACAGCCAGAGCCAAGAAGCC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                    GGCTGTGCTGCAGGCACAGGGTGCCCCTGTCCAGCCCCTCCACCTGTGTCTGAATGCAAC 773
                                                                                                                                                                                                                                                                                                                                                                        TGGCTAAGAAAAAAAGCTGGAAAAAGAAGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAGGCGAGCG 547
AGGGGTGTTGTGGGGGGCAACACTAAAGTCCCTCACCCCCGACTCTCCAGGTGGAGG
                                                                                                                                                                                                                               AGGATTCAAGAAATGAGGAGCCACGCCTTGGGGGGGCACGGTGCAAAGTGGGCCCTTCCCCTG 713
                                                                                          GGCTGTGCTGTGGGTGCAGGATGC------CCCCTCCATCTGTGTCTGAATATGAC
                                                                                                                                                                                                                                                                             TAGTGTTAGAGGCAAGAGCCCTTGGAAATAGGCCAAACACACATTCAGGCC----- 15998
                                            AGGGGTGTTGCGGGGGCAACATGAGAGCCCCCTCACCCCCAACTCTCCACTTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                   CAAGAAATGAGGAGCCATGCCTTGGAGGTCATGGTGCAGAGTGAACCTGCCCCT 15944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 171.6;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 86574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            --- AGAGGAAATAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Gaps
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exon
misc_feature
                        intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 14; human chromosome 8p21; contraceptive; gynaecology; cancer; cell proliferative disorder; cell degenerative disorder; ovulation; modulator; human infertility; signalling pathway; screen; treatment; ds.
                                                                                                                                                                                                                                                                                                                                                                                     intron
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/number=
980
                      /*tag= s
/number= 6
965..995
                                                 /*tag= r
/note= "Corresponds
~f intron 5 between
                                                                                                                                                                                         /number- 4
657..687
                                                                                                               /*tag= p
/number= 5
                                                                                                                                                                                                                                                                                                                            1ntron 2
426..511
                                                                                        /*tag= q
/number= 5
                                                                                                                              /*tage o
/note= "Corresponds to 2771 (2.77kb) missing nucleotides
of intron 4 between bases 671 and 673"
                                                                                                                                                                                                                 intron 3 between 543..656
                                              of intron 5
813..964
                                                                                                                                                                       /number-
                                                                                                                                                                                                                      /note- "Corresponds to 63 missing nucleotides intron 3 between bases 526 and 528"
                                                                                                                                                                                                                                                                          512..542
                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= e
/number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number= 1
200..230
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151..199
               /*tag=
                                                                                                                                                                                                                                                           /number- 3
                                                                                                                                                                                                                                                                                                                                                                                     395..425
                                                                                                       782..812
                                                                                                                                                                                                                                                                                   /noté= "The
                                                                                                                                                                                                                                                                                                            /number- 3
                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/number= 2
                                                                                                                                                                                                                                                                                                                                                                                          /product= "Mouse ovary-specific Npm2/note= "Coding region is interrupted
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Corresponds to 314 missing nucleotides of intron 1 between bases 214 and 216"
                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                  "Corresponds to 105 missing nucleotides 2 between bases 409 and 411"
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                                                                                                                                                                                                                                                                                   Η,
                                                                                                                                                                                                                                                                                  is replaced with 'G'
                                                      to 1321 (1.32kb) missing nucleotides bases 796 and 798"
                                                                                                                                                                                                                                                                                  in the
                                                                                                                                                                                                                                                                                                                                                                                          protein"
by 8 introns"
                                                                                                                                                                                                                                                                                  CDNA"
                                                                                                                                                                                                                                of.
                                                                                                                                                                                                                                                                                                                                          of.
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The present sequence is the mouse ovary-specific Npm2 gene, mapped to C the middle of mouse chromosome 14. It shows linkage to Dl4Mit32, this CC region being syntenic to human chromosome 8p21. The clone 01-236 cDNA is C used to screen and identify Npm2 gene. It is the mammalian ortholog of C Xenopus laevis nucleoplasmin (Xnpm2) expressed exclusively in the eggs. CC It provides in vitro and in vivo reagents for studying ovarian CC contraceptive activity. Agents which modulate 01-180, Ol-184 and Ol-236 CM ay be used to treat cell proliferative or degenerative disorders, CC contraceptive activity. Agents which modulate 01.236 CM associated with abnormal expression of these ovary specific genes. This CC contraceptives, to block ovulation in a reversible manner. It is also CC used to screen for genetic mutations in signalling pathways, that is associated with some form of human infertility or gynaecological cancer. Yxx
                                                                                                                                                                                                                                     \rm O1\text{-}180 , \rm O1\text{-}184 and \rm O1\text{-}236 polypeptides and nucleic acids encoding them, useful for evaluating potential contraceptives to block ovulation in a reversible manner -
 Sequence 1481 BP; 407 A; 379
                                                                                                                                                                                                               Example 5;
                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                 WPI; 2000-350684/30
                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                          Matzuk MM, Wang P;
                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
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                                                                                                                                                                                                              Fig 13;
                                                                                                                                                                                                                                                                                                                                                                            98US-0106020
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1117
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25209
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/note= "The
1361..1366
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996..1036
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1382...
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1037..1067
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/note= "Corresponds to
. . . . . A between bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Corresponds to 63 missing nucleotides intron 8 between bases 1116 and 1118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Corresponds to 471 missing nucleotides
intron 7 between bases 1051 and 1053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′*tag=
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                                                                                                                                                                                                             English.
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391 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is replaced with 'T' in the cDNA"
296 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 missing nucleotides 979 and 981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
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Query Match

14.2%;

Score 131.6;

DB 21; Length 1481;

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DЬ
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Matches
31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-APR-2000

19-MAY-2000

07-JUN-2000

07-JUN-2000

07-JUL-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000
                                                                                                                                                                                                                                                                                                                             02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human reproductive system related antigen cDNA SEQ ID NO: 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL01804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL01804 standard; cDNA; 416 BP
                                                                                                                                                                                                                                                                                             17-JAN-2001;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                          The present invention provides the protein and coding sequences of number of human reproductive system related antigens. These can be in the prevention and treatment of, reproductive system disorders, including cancer. The present sequence is a coding sequence of the
                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
17-NOV-2000;
                                              Sequence 416 BP;
                                                                                                                                                                                           P-PSDB; AAM95834
                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
17-NOV-2000;
                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antig is used in preventing, treating or ameliorating a medical condition
                                                                  invention.
                                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                    2001-465570/50.
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          7.8%;
50.0%;
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Score 72.4; DE Pred. No. 8.2e: 1; Mismatches
  1:
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                    Human; testicular antigen; testes; cancer; metastasis; immune disorde reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human testicular antigen encoding cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL97097
                                                                                                                                                                                                                                                                                                              02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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17-NOV-2000
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                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the
                                                                                                                                                                                                     Sequence 416
                                                                                                                                                                                                                                                                                                                                                                                      Claim
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111 TTGGACCTTCAGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGCTTCATACGAT
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                                                                                                                                             7.8%;
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Pred. No. 8.2e
1; Mismatches
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2000US-0232981
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                  The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, ospecially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described in the method of the invention.
                                                                                                                                      bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity.
                                                                                                                                                                                         This invention describes novel nucleic acids (I; designated LOBO (long
                                                                                                                                                                                                                               Example 3; Page 69-97; 391pp; German.
                                                                                                                                                                                                                                                                Nucleic acids encoding proteins which influence bone development,
                                                                                                                                                                                                                                                                                                                      WPI; 1999-601320/51
                                                                                                                                                                                                                                                                                                                                                         Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                          (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 TTCTGGCCCTGTGCGGNTCANTGGGCGGCACCAGATTGTTACGATGAGCAATGATGTTTC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 CTCAGGACCCGTGTTCCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGA 410
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Query Match

Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 other;

7.68;

Score 70.2;

DB 20;

Length 49999,

Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209

T; 0 other;

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                                development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine Loud protein desyribed in the marked of the increase.
                                                                                                                                          This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e.
                                                                                                                                                                                                                                         Nucleic acids encoding proteins which influence bone development, wasful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                          in the method of the invention.
                                                                                                                                                                                                            Example 3; Page 161-189; 391pp; German.
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0; Mismatches 128;
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   Query Match 7.6
Best Local Similarity 53.9
Matches 147; Conservative
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16-MAR-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21883.
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Pred. No. 1.3e-06;
0; Mismatches 128;
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08-DEC-2000
                                                                                                                                                   Disclosure; SEQ ID NO 21883; 3071pp + Sequence Listing; English
                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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11-DEC-2000;
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2000US-0251990.
2000US-0254097.
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2000US-0256719.
2000US-0251479.
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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally. (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK87930 and AAM82169 represent sequences used in the exemplification of the present

Sequence 33923 BP; 9925 A; 8140 C; 7946 G; 7912 T; 0 other;

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Matches 122; Conservative
                  Local Similarity
             7.5%;
58.1%;
   0; Mismatches
 Score 69.2; DB 22;
Pred. No. 2e-06;
0; Mismatches 88;
  Indels
                         Length 33923;
  0;
Gaps
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0

The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful in medical cCC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC dispositics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94544 represent novel human RESULT 11 AAS90676 B Вb δã 밁 Ş Ωy В 23000 AGGAGAAGGAGGAGAAGGAGAAGGAGA 23029 diagnostic coding sequences of the invention. Claim 1; SEQ ID No 26480; 103pp; English. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity Drmanac RT, Liu C, 31-MAR-2000; 23-AUG-2000; P-PSDB; (HYSE-) HYSEQ INC. 30-MAR-2001; 2001WO-US08631 11-OCT-2001. Homo sapiens AAS90676 standard; cDNA; 341 Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder; DNA encoding novel human diagnostic protein #26480 13-FEB-2002 AAS90676; 497 377 2001-639362/73. AGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAAGAAGAAGAAGGGGAGG AAAAAAAGCTGGAAAAAGAAGAAGAAGAAA AAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAGGCGAGCGTGGCTAAGA 556 AGGAGGAAGAGGAAGAAGATGATGAGGATGAGGATGCAGATATATCTCTGGAGGAGC 496 ABG26489 2000US-0540217 2000US-0649167 (first entry) YT; forensic; mutations 436 22879

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RESULF 12
ARG54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HTLEP21 cDNA, SEQ ID NO:577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2002
                                                          Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping;
antibody preparation; cytostatic;
   neurological diseases
                                ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                           Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                07-JUN-2000; 2000US-209467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; gynaecological;
                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 GAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAAGAAGAAGGGGGAGGAGGAAGAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 AGAAGAAGAAGAAGAAGAAGAAACAACTTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                568 GAAAAAGAAGAAGAAGAATAAGAGCCAGCGTTAGAGACAAGAGCCCTGTGAAAAAAGGCC
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55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic analysis;
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Claim 1; SEQ ID No 577; 2922pp; English

metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which invention.

at ftp.wipo.int/pub/published\_pct\_sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Sequence 512 BP; 116 A; 137 C; 154 G; 99 T; 6 other;

Matches Query Match Local Similarity 207; Conservative 7.3%; 50.4%; უ ლ Score 67.8; Pred. No. 1 Mismatches 192; .1e-06 DB 24; Indels Length 512; 7; Gaps

QУ Вb 111 TTGGACCTTCAGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGAT 170 N GCACGAGGAGGGTGGTACTGGGGCGGTAASAGGCTGTGAGCTCTCCGGCCACACCCGCTC 61

Ъ 62 CTTCACCTTTAAGGTAGAGGAAGAGGATGATGCG-GMMRCGTGCTGGCACTAACCATGCT 120

Q TTGCTTGGGGGAGAAAGCCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAA 230

Ъ CTGCCTCACCGAGGGAGCCAAAGACGAGTGTAATGTGGTAGAAGTTGTGGCCC-----G 174

В Qy

QΥ 291 CATGGTCTCCATGGTAGGAGTGCAGCTTTCTCCCCCAGTTACTTTCCAGCTCCGGGCTGG 350

В 235 CATGCTCAGTCTGGATGACTTCCAGCTCCAACCACCTGTAACCTTCCGCCTGAAGTCGGG

B QУ 351 CTCAGGACCCGTGTTCCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGA 410 YTCTGGCCMTGTGCGGATCACTGGGCGGCACCAGATTGTTACGATGAGCAATGATGTTTC

ΧĦ AAS68926 RESULT 13 AAS68926 standard; cDNA; 291 BP

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                                                                                                                                                                                                                                                                                                                                    CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC and gene mapping, and in recombinant production of (II). The
CC and gene mapping, and in recombinant production of (II). The
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in disgnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating annibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC The polypeptide and polynucleotide sequences have applications in
CC anino stics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC anino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC at fits.wiso.int/sub/sublished not secuence format directly from WIPO
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        Sequence 291 BP; 129 A; 22 C; 112 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 4730; 103pp; English.
                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
362 TGTTCCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGG 421
                                  482 TATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAGG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #4730
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                                                                                                                                                        8
                                                                      TTTGCCATATTGGCCAGGCTAGTCTCGAACTCCTGACCTCAGGGGAGGAAGAGGAGGAAG 67
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                           54.0%;
                                                                                                                                                                                                                    Score 66.4; DB 23; Length 291;
Pred. No. 2e-06;
0; Mismatches 116; Indels 0
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                Gaps
   187
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CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (C (II). (II) is useful for generating antibodies against it, detecting or cquantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cdisorders involving aberrant protein expression or biological activity. (I) and to produce and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polynucleotide sequences have application of mutations can do produce other types of data and products dependent on DNA and consisting and to produce other types of data and products dependent on DNA and consisting and sequences. AAS4197-AAS94564 represent novel human consisting the formation, but was obtained in electronic format directly from WIPO as formation, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags in the polynucleotides.
                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 4342; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Query Match

Sequence 1680 BP; 574 A; 286 C; 485 G; 335 T; 0 other;

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AAK82672/c
ID AAK82672 standard; DNA; 8165
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    Best Local Similarity Matches 115; Conserv
18-APR-2000;
19-MAY-2000;
28-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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14-JUL-2000;
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14-AUG-2000;
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24-FEB-2000;
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16-MAR-2000;
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cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0180628.
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2000US-0186350.
2000US-0189874.
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2000US-019076.
2000US-0205515.
2000US-0205467.
  2000US - 0214886.
2000US - 0215135.
2000US - 021647.
2000US - 0216880.
2000US - 0217487.
2000US - 0218290.
2000US - 02217496.
2000US - 0220963.
2000US - 0224518.
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2000US - 0225214.
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2000US - 0225266.
2000US - 0225266.
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01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
14-SEP-2000;
           29-SEP-2000
02-OCT-2000
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                                                                                                                                                                                    expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic antigen genomic to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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                                3706 GCAGTGAACCGAGATCACACCACTGCTCTCCAGCCCAGGTAACAGAGCCAGACTCCATCT 3647
                                                                                                                                                           Sequence 8165 BP; 1595 A; 2353 C; 2025 G; 2192 T; 0 other;
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01-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 37484; 3071pp + Sequence Listing; English.
367 CTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACCTGGGAGGAGGAGGAGGAAGAA 426
                                                              Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483426/52.
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## ALIGNMENTS

	TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	ALISTIA ALIST ALIS
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.  CDNA Library Preparation: M. Bento Soares, Ph.D.  CDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  www-bio.llni.gov/bbrp/image/image.html  Seq primer: -40UP from Gibco	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D.	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 517) NCI-GGAB http://mai.och.och.och.och.och.och.och.och.och.och	AI391464 S17 bp mRNA linear KST 02-FEB-1999 tt96905.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107160 3' sequence. Sequence. AI391464 AI391464 AI391464 AI391464 AI391464.1 GI:4217468

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ot78a10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1622874 3' similar to contains element MER22 repetitive
 Homo sapiens
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                          human
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                                                                   AI016313
                                                                                element ;, mRNA sequence
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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/tissue_type="B-cell, chronic lymphotic leukemia"
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/db_xref="taxon:9606"
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                                            CTCGGGGTCACAATAAAGTTGCCTGGTCAGGAAAA 887
                                                                                       CATGAGAGCCCCTCACCCCCAACTCTCCACTTTCAGGAGGCCCCCAGTGAAGAGCCCCAC
                                                                                                              CATGAGAGCCCCTCACCCCCAACTCTCCACCTTTCAGGAGGCCCCCAGTGAAGAGCCCCAC 852
                                                                                                                                                                                GGTGCCCCTGTCCAGCCCCTCCACCTGTGTCTGAATGCAACAGGGGTGTTGCGGGGGCAA
                                                                                                                                                                                                                        GGTGCCCCTGTCCAGCCCCTCCACCTGTGTCTGAATGCAACAGGGGTGTTGCCGGGGGCAA 792
                                                                                                                                                                                                                                                                     GCCACGCCTTGGGGGGCACGGTGCAAAGTGGGCCTTCCCTGGGCTGTGCTGCAGGCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov) for further information.
INSort Length: 1368 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
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Pred. No. 1.4e-66;
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                             451 GAGGAAGATGATGAGGATGAGGATGCAGATATATCTCTGGAGGAGGAAGCCCTGTCAAA 510
                                                                                                                                                        Local
GAGGAAGATGATGAGGATGAGGATGCAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAA 120
                                                                                                       433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.linl.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-805; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by
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/clone="IMAGE:5674315"
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                                                                                                                                                                                                                                                                                                                                    Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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                  /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA
                                                                                                 /lab_host-"DH10B"
                                                                                                                           /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
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                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:5674315"
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                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      Tissue Procurement: ATCC
                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 432.2; DB 1
Pred. No. 8.9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 05-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE: 5454702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 ACGATTTGCTTGGGGGAGAAAGCCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286
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                                                                                                                                                                                              586 ATAAG-AGCCAGCGTTAGAGACAAGAGCCCTGTGAAAAAGGCCAAAGCCACAGCCAGAGC 644
                                                                                                                                                                                                                                                                                                                                                      466 GATGAGGATGCAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTG
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600 GGAAAAGGGGGGGGGNNGGGGNAGGGGGGGGG 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGGACTTGGACCTTCAGACCCCAGCTGGAGGGGAAGCAGAGCTGCTGCAGGCTGTTCAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCCCATGGTCTCCATGGTAGGAGTGCAGCTTTCTCCCCCCAGTTACTTTCCAGCTCCGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAACCAGGAGGACAAGAAGATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTC 285
                                                                                                                                                                                                                                                                                                                                                                                               TGGGAGGAGGAGGAAGAAGAAGAGGGGAGGAGGAAGAGGAANANGAANANGANNAN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGCTCAGGACCCGTGTTCCTCAGTGGCCAGGAACGTTATGAAGCATCAGACCTAACC 405
                                                                                                                                                         GNAAGAAAGGAGGGGAGAAAAAGAGGNGGGGGAAGAGAGGNAAAGNNAGAGGGAAGA
                                                                                                                                                                                                                                                                           GTGCCCCAGAAGCAGGCGAGCGTGGCTAAGAAAAAAAAGCTGGAAAAAGAAGAAGAAGAAGAA
                                       CCTTCCCTGGGCTGTGCTGCAGGCACAGGG 734
                                                                            CAAGAAGCCAGGATTCAAGAAATGAGGAGCCACGCCTTGGGGGGCACGGTGCAAAGTGGG 704
                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: POTB4; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5; adaptor: GGCACCAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2Ap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5454702"
/clone_lib="NIH_MGC_98"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="DH108 (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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78.4%;
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                                                                                                                                                                                                                                   181 GAGAAAGCCAAAGAGGAGATGCATCGCGTGGAGATCCTGCCCCCAGCAAACCAGGAGGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                                                                                                                                                                               267 GCAGTGACNNCCGTGCTCTGGGGCTGCGAGCTCAGTCAGGAGAGGCGGACTTGGACCTTC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCCCGCTTCTCTGCCCCGGAGCCATGAATCTCAGTAGCGCCAGTAGCACGGAGGAAAAG 60
ATGGTAGGAGTGCAGCTTTCTCCCCCAGTTACTTTCCAGCTCNNNGCTGGCTCAGGACCC 566
                                                                                                                                                                                                                                                                                                           AGACCCCAGCTGGAGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGATTTGCTTGGGG 180
                                          AAGAAGATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTCCTCCCCATGGTCTCC 506
                                                                                                                                      AAGAAGATGCAGCCGGTCACCATTGCCTCACTCCAGGCCTCAGTCCTCCCCATGGTCTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCCGCTTCTCTGCCCGGAGCCATGAATCTCAGTAGCGCCAGTAGCACGGAGGAAAAG 266
                                                                                                                                                                                           GAGAAAGCCAAAGAGGAGATGCATCGNNTGGAGATCCTGCCCCCAGCAAACCAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGTGACGACCGTGCTCTGGGGCTGCGAGCTCAGTCAGGAGGGGGGGACTTGGACCTTC 120
                                                                                                                                                                                                                                                                                       AGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGATTTGCTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov plate: LLCM2324 row: 1 column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence.
BQ878692
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 854)
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/db_xref="taxon:9606"
/clone="IMAGE:6087706"
/clone=libb="NIH_MGC_112"
/tissue_type="melanotic melanoma, cell line"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; vector: poTB7; Site_1: xhoI; Site_2:
EcoRI; cDNA made by oligo-dT prining. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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a 247 c 253 g
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2333 row: f column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                         /tissue_type="melanotic melanoma, cell line"
/lab_host="bHl0B (phage_resistant)"
/note="Organ: skin; Vector: pOTDF; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT prining. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACCAMG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
NIH_MGC Library."
283 c 277 g
                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:6091012"
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                                                                                                                                                    --GTTGCGGGGGCAACATG-AGAGCCCCTCACCCCCAACT 816
                                                                                                                                                                          CTGCAGGCACAGGGTGCCCCTGTCCAGCCCCCTCACCTGTGTCTGAAATGCACNGGGGNT 818
 Homo sapiens
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EST.
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                                                                           BQ878312
                                                     AGENCOURT_8072779 NIH_MGC_112
5', mRNA sequence.
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77.08;
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                                                                  Homo sapiens cDNA clone IMAGE: 6087652
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ATATCTCTGGAGGAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAG
                                                                                          GTGTTCCTCAGTGGCCAGGAACGTTAT-----
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
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High quality sequence stop: 548.
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76.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repetitive element ;, mRNA sequence. BF594409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to contains Alu repetitive element; contains element MER28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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7105a05.xl NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3324560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              info@image.llnl.gov
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              54
                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 404.
/note-*Organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive purification reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:3324560"
                                                                                                                                                                                                                                                               /tissue_type="colon tumor, RER+"
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Co16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 CACAGGGTGCCCCTGTCCAGCCCTCCACCTGTGTCTGAATGCAACAGGGGTGTTGCGGG
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                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence.
AW731946
                                                                                                                                                                                                                                                                                             High quality sequence stop: 381.
                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 399)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgapbs-r@mail.nih.gov
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                               /db_xref="taxon:9666"
/clone="IMAGE:2823298"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                               ∕organism≖"Homo sapiens"
                                                                                                                                                                                                                                                                           LOCAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 GAGCAAAGCCCTGTCAAACAAGTCAAAAGGCTGGTGCCCCAGAAGCAGGCGAGCGTGGCT 340
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BQ684424.1 GI:21797103
EST.
                                                                                                                                               cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                               High quality sequence stop: 635
                                                                                                                                     Plate: LLCM2419 row: k column:
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                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 935)
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                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 116 c 108 g 122 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6260492"
/clone_lib="NIH_MGC_112"
                                                                              1. .935
                                                                                             Location/Qualifiers
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 397.4; DB 1 Pred. No. 5.9e-57;
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ORIGIN
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM24L5 row: o column: 16
High quality sequence stop: 518.
                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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5', mRNA sequence.
                                                                                                                                                                                                                                        Unpublished (1999)
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/lab_host="bH10B (phage-resistant)"
/note="organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="congly.hol sites using the following 5 adaptor:
into EccRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
86 a 304 c 269 g 175 t 1 others
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98.7%;
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                                                                                                                                                                                                                                                                          476 CAGATATATCTCTGGAGGAGCAAAGCCCTGTCAAAACAAGTCAAAAGGCTGGTGCCCCAGA 535
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                                               GATTCAAGAAATGAGGAGCCCCCGCCTTGGGGGGGCACGGTGCAAAGTGGGCCTTCCCCT 759
                                                                                GATTCAAGAAATGAGGAGCCAC--GCCTTGGGGGGCACGGTGCAAAGTGGGCCTT-CCCT 712
                                                                                                                GCGTTAGAGACAAGAGCCCTGTGAAAAAGGCCAAAAGCCCACAGCCAGAGCCAAGAAGCCAG
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AGACCCCAGCTGGAGGGGAAGCAGAGCTGCAGGCTGTTGCTTCATACGATTTGCTTGGGG
                                                                                                                                                                               ------GAAAAAAAGCTGGAAAAAGAAGAAGAAGAATAAGAGCCA
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/lab_host="DHIOB (phage=resistant)"
/note="organ: skin; Vector: pOTBP; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5; adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

159 t 7 others
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74.0%;
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Pred. No. 6.5
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Insert Length: 431 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
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/Clone="IMAGE:2524500"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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                                                                                                                           38.7%;
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Contact: Robert Strausberg, Ph.D.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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/lab_host="DH10B"
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/clone="IMAGE:3442494"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 AGAAGCAGGCGAGCGTGGCTAAGAAAAAAAAAGCTGGAAAAAGAAGAAGAAGAAATAAGAG 302
                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        773 CAGGGGTGTTGCGGGGGCAACATGAGAGCCCCTCACCCCCAACTCTCCACTTTCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GGGCTGTGCTGCAGGCACAGGGTGCCCCTGTCCAGCCCTCCACCTGTGTTTGAATGCAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CAGGATTCAAGAAATTAGGAGCCACGCCTTGGGGGGCCACGGTGCAAAGTGGGCCTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 CAGGATTCAAGAAATGAGGAGCCACGCCTTGGGGGGCACGGTGCAAAGTGGGCCTTCCCT 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF057162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF057162 361 bp mRNA linear EST 10°CL'-20
7k16g07.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3444661 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF057162.1 GI:10811058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                        Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                          cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                  info@image.llnl
                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                            Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
polylinker; Site_1: Not I; Site_2:
    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DN
                                                                                        /clone="IMAGE:3444661"
/clone_lib="NCI_CGAP_GC6"
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                            ocation/Qualifiers
                                                                                                                                                                                     . 361
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99.4%;
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 Mismatches

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Pred. No. 2.5e-50;
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BASE COUNT
ORIGIN
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Best Local Similarity 99.4%;
Matches 359; Conservative
                                                                     121 CAGGGGTGTTGCGGGGGCAACATGAGAGCCCCCTCACCCCCAACTTTCCACTTTCAGGAGG 62
                                                                                                                                                                                                                                      893 A 893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the normalized library NCI_CGAP_GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 107 c 93 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Pred. No. 2.5e-50;
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